

From: Chan, Christina
Sent: Thursday, March 13, 2003 11:46 AM
T : Seharaseyon, Jegatheesan; STIC-Biotech/ChemLib
Subject: RE: RUSH Search Of 09/700590

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Seharaseyon, Jegatheesan
Sent: Thursday, March 13, 2003 9:32 AM
To: Chan, Christina
Cc: O'Bryen, Barbara
Subject: RUSH Search Of 09/700590
Importance: High

Hi,
Please rush this search for me. Thanks.

1. Search the nucleotide encoding SEQ ID NO: 22 in the commerical database.
Also compare seq id no: 22 TO Acc. NO: CAA72780.1, AAC27978.1, CAA66186.1.

Thanks

J.Seharaseyon
Art Unit 1647
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Point of Contact:
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 22vspep2.res made by shanley on Mon 17 Mar 103 12:31:25-PST.

Query sequence being compared:	US-09-700-590A-22 (1-688)
Number of sequences searched:	1
Number of scores above cutoff:	1

Results of the initial comparison of US-09-700-590A-22 (1-688) with:
File : sehpep2.pep

PARAMETERS

Similarity matrix	Unitary	K-tuple	3
Mismatch penalty	6	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	70	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	128
Number of sequences searched:	1
Number of scores above cutoff:	1

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
1. caa66186	TOIG of: caa66186	205	128	70
		check: 205	128	70
				0.00 0

1. US-09-700-590A-22 (1-688)
caa66186 TOIG of: caa

Initial Score	=	70	Optimized Score	=	70	Significance	=	0.00
Residue Identity	=	75%	Matches	=	70	Mismatches	=	23
Gaps	=	0	Conservative Substitutions	=	0		=	0

X 600 610 620 630 640 650 660
 PPTYEEDKKPMSYEBKRLQSLDINKLPGCKLGRVVHIQSRPSLKNNSPDEIEIETFETLKPSTLREL
 PPTYEEDKKPMSYEBKRLQSLDINKLPGCKLGRVVHIQSRPSLKNNSPDEIEIETFETLKPSTLREL
 PPTYEEDKKPMSYEBKRLQSLDINKLPGCKLGRVVHIQSRPSLKNNSPDEIEIETFETLKPSTLREL
 X 10 20 30 40 50 60 70

670 680 X
GALCHLLFAEEKETFKLRKLM

ERYVTSCLRKKRKPQAEKVDV
80 90 X

